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1645

RAW SEQUENCE LISTING

DATE: 02/12/2002

PATENT APPLICATION: US/09/976,451

TIME: 12:05:54

Input Set : A:\Pm4968.txt

Output Set: N:\CRF3\02122002\I976451.raw

P.S

ENTERED

4 <110> APPLICANT: Braun, Jonathan
5 Wei, Bo
6 Forbes, Ashley
8 <120> TITLE OF INVENTION: Methods of Diagnosing and Treating
9 Crohn's Disease Using Pseudomonas Antigenes
12 <130> FILE REFERENCE: P-PM 4968
14 <140> CURRENT APPLICATION NUMBER: US 09/976,451
15 <141> CURRENT FILING DATE: 2001-10-12
17 <150> PRIOR APPLICATION NUMBER: US 60/240,347
18 <151> PRIOR FILING DATE: 2000-10-13
20 <160> NUMBER OF SEQ ID NOS: 10
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 551
26 <212> TYPE: DNA
27 <213> ORGANISM: P. fluorescens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)...(549)
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35 Met Thr Glu Pro Val Ser Thr Gly Arg Cys Asp Ser Pro Leu Leu Gln
36 1 5 10 15
38 gcg ttc gtc gac aat cga ctg att ctg gtg aag atc gcg gcc cgt atc 96
39 Ala Phe Val Asp Asn Arg Leu Ile Leu Val Lys Ile Ala Ala Arg Ile
40 20 25 30
42 acc ggg tgc cgc tcc cgc gcc gaa gac gtg gtg cag gac gcc tac ttc 144
43 Thr Gly Cys Arg Ser Arg Ala Glu Asp Val Val Gln Asp Ala Tyr Phe
44 35 40 45
46 cgg ctg cag tcg gcg ccg acc atc acc tca tcg ttc aag gcc caa ctg 192
47 Arg Leu Gln Ser Ala Pro Thr Ile Thr Ser Ser Phe Lys Ala Gln Leu
48 50 55 60
50 agt tat ctg ttt cag atc gta cgc aac ctg gcg atc gat cat tac cgc 240
51 Ser Tyr Leu Phe Gln Ile Val Arg Asn Leu Ala Ile Asp His Tyr Arg
52 65 70 75 80
54 aag cag gcc ctg gag ctc aaa tac tcc ggg acc gaa gag gaa ggc ttg 288
55 Lys Gln Ala Leu Glu Leu Lys Tyr Ser Gly Thr Glu Glu Glu Gly Leu
56 85 90 95
58 aat gtg gtt att cac ggc gct tca ccg gaa acc tcg cac atc aat ttc 336
59 Asn Val Val Ile His Gly Ala Ser Pro Glu Thr Ser His Ile Asn Phe
60 100 105 110
62 aac acc ctg gaa aac atc gcc gac gcc ctg acg caa ctg ccc cag cgc 384
63 Asn Thr Leu Glu Asn Ile Ala Asp Ala Leu Thr Gln Leu Pro Gln Arg

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TECH CENTER 160012900

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64          115          120          125
66 acc cgc tac gcg ttc gag atg tac cgc ttg cat ggc gtg ccg caa aaa 432
67 Thr Arg Tyr Ala Phe Glu Met Tyr Arg Leu His Gly Val Pro Gln Lys
68      130          135          140
70 gac atc gcc aag gag ctt ggg gtg tct ccg acc ttg gtg aac ttc atg 480
71 Asp Ile Ala Lys Glu Leu Gly Val Ser Pro Thr Leu Val Asn Phe Met
72 145          150          155          160
74 att cgc gat gcg ctg gtg cat tgc cgc aag gtg tcg ggc agt cat agc 528
75 Ile Arg Asp Ala Leu Val His Cys Arg Lys Val Ser Gly Ser His Ser
76          165          170          175
78 gat acg ttt gcg cgg cgg gtt ta 551
79 Asp Thr Phe Ala Arg Arg Val
80          180
83 <210> SEQ ID NO: 2
84 <211> LENGTH: 183
85 <212> TYPE: PRT
86 <213> ORGANISM: P. fluorescens
88 <400> SEQUENCE: 2
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90 1          5          10          15
91 Ala Phe Val Asp Asn Arg Leu Ile Leu Val Lys Ile Ala Ala Arg Ile
92      20          25          30
93 Thr Gly Cys Arg Ser Arg Ala Glu Asp Val Val Gln Asp Ala Tyr Phe
94      35          40          45
95 Arg Leu Gln Ser Ala Pro Thr Ile Thr Ser Ser Phe Lys Ala Gln Leu
96      50          55          60
97 Ser Tyr Leu Phe Gln Ile Val Arg Asn Leu Ala Ile Asp His Tyr Arg
98 65          70          75          80
99 Lys Gln Ala Leu Glu Leu Lys Tyr Ser Gly Thr Glu Glu Glu Gly Leu
100          85          90          95
101 Asn Val Val Ile His Gly Ala Ser Pro Glu Thr Ser His Ile Asn Phe
102          100          105          110
103 Asn Thr Leu Glu Asn Ile Ala Asp Ala Leu Thr Gln Leu Pro Gln Arg
104          115          120          125
105 Thr Arg Tyr Ala Phe Glu Met Tyr Arg Leu His Gly Val Pro Gln Lys
106      130          135          140
107 Asp Ile Ala Lys Glu Leu Gly Val Ser Pro Thr Leu Val Asn Phe Met
108 145          150          155          160
109 Ile Arg Asp Ala Leu Val His Cys Arg Lys Val Ser Gly Ser His Ser
110          165          170          175
111 Asp Thr Phe Ala Arg Arg Val
112          180
115 <210> SEQ ID NO: 3
116 <211> LENGTH: 184
117 <212> TYPE: PRT
118 <213> ORGANISM: P. fluorescens
120 <400> SEQUENCE: 3
121 Met Thr Glu Gln Val Ser Thr Ser Lys Cys Asp Ser Pro Leu Leu His
122 1          5          10          15

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123 Ala Phe Val Asp Asn Arg Leu Ile Leu Val Lys Ile Ala Ala Arg Ile
124           20           25           30
125 Thr Gly Cys Arg Ser Thr Ala Glu Asp Val Val Gln Asp Ala Phe Phe
126           35           40           45
127 Arg Leu Gln Ser Ala Pro Pro Ile Thr Ser Ser Ile Lys Ala Gln Leu
128           50           55           60
129 Ser Tyr Leu Phe Gln Ile Val Arg Asn Leu Ala Ile Asp His Tyr Arg
130 65           70           75           80
131 Lys Gln Ala Leu Glu Gln Lys Tyr Ser Gly Pro Glu Glu Glu Gly Leu
132           85           90           95
133 Asn Val Val Ile Gln Gly Ala Ser Pro Glu Thr Ser His Ile Asn Phe
134           100          105          110
135 Ser Thr Leu Glu Asn Ile Ala Asp Ala Leu Thr Glu Leu Pro Ser Arg
136           115          120          125
137 Thr Arg Tyr Ala Phe Glu Met Tyr Arg Leu His Gly Val Pro Gln Lys
138           130          135          140
139 Asp Ile Ala Lys Glu Leu Gly Val Ser Pro Thr Leu Val Asn Phe Met
140 145          150          155          160
141 Ile Arg Asp Ala Leu Val His Cys Arg Lys Val Ser Gly Ser Arg Arg
142           165          170          175
143 Asp Ala Val Ala Val Gly Arg Arg
144           180

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147 <210> SEQ ID NO: 4

148 <211> LENGTH: 597

149 <212> TYPE: DNA

150 <213> ORGANISM: P. fluorescens

152 <220> FEATURE:

153 <221> NAME/KEY: CDS

154 <222> LOCATION: (1)...(594)

156 <400> SEQUENCE: 4

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157 atg cgc acc atg gtc gac agt ggc caa ttg acc gac ccc gag agc gcc 48
158 Met Arg Thr Met Val Asp Ser Gly Gln Leu Thr Asp Pro Glu Ser Ala
159 1           5           10           15
161 cgc ggc aag ttg ctg caa acc gcg gct cat ctg ttt cgc aac aag ggt 96
162 Arg Gly Lys Leu Leu Gln Thr Ala Ala His Leu Phe Arg Asn Lys Gly
163           20           25           30
165 ttc gag cgc acc acc gtg cga gat ctg gcc agc gcc gtg ggc atc cag 144
166 Phe Glu Arg Thr Thr Val Arg Asp Leu Ala Ser Ala Val Gly Ile Gln
167           35           40           45
169 tcc ggc agc atc ttt cat cac ttc aag agc aag gat gag ata ttg cgt 192
170 Ser Gly Ser Ile Phe His His Phe Lys Ser Lys Asp Glu Ile Leu Arg
171           50           55           60
173 gcc gtg atg gag gaa acc acc cat tac aac acc gcg atg atg cgc gct 240
174 Ala Val Met Glu Glu Thr Thr His Tyr Asn Thr Ala Met Met Arg Ala
175 65           70           75           80
177 tca ctg gaa gaa gcg agc acg gtg cgc gaa cgc gtg ctg gcg ctg atc 288
178 Ser Leu Glu Glu Ala Ser Thr Val Arg Glu Arg Val Leu Ala Leu Ile
179           85           90           95
181 cgc tgc aag ttg cag tcg atc atg ggc ggc agt ggc gag gcc atg gcg 336

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182 Arg Cys Lys Leu Gln Ser Ile Met Gly Gly Ser Gly Glu Ala Met Ala
183          100          105          110
185 gtg ctg gtc tac gaa tgg cgc tcg ctg tcg gcc gaa ggc cag gcg cac 384
186 Val Leu Val Tyr Glu Trp Arg Ser Leu Ser Ala Glu Gly Gln Ala His
187          115          120          125
189 gtg ctg gcc ctg cgt gac gtg tat gag cag atc tgg ttg cag gta ctg 432
190 Val Leu Ala Leu Arg Asp Val Tyr Glu Gln Ile Trp Leu Gln Val Leu
191          130          135          140
193 ggc gag gcc aag gcc gct ggc tac atc cgg ggc gac gtg ttt att acc 480
194 Gly Glu Ala Lys Ala Ala Gly Tyr Ile Arg Gly Asp Val Phe Ile Thr
195 145          150          155          160
197 cgg cgc ttc ctc acc ggg gcc tta tcc tgg acc acc acc tgg ttt cgt 528
198 Arg Arg Phe Leu Thr Gly Ala Leu Ser Trp Thr Thr Thr Trp Phe Arg
199          165          170          175
201 gcc caa ggc agc ctg acc ctt gag gag ttg gcc gaa gag gcc ttg ttg 576
202 Ala Gln Gly Ser Leu Thr Leu Glu Glu Leu Ala Glu Glu Ala Leu Leu
203          180          185          190
205 atg gtg ctg aag tcg gac tga 597
206 Met Val Leu Lys Ser Asp
207          195
210 <210> SEQ ID NO: 5
211 <211> LENGTH: 198
212 <212> TYPE: PRT
213 <213> ORGANISM: P. fluorescens
215 <400> SEQUENCE: 5
216 Met Arg Thr Met Val Asp Ser Gly Gln Leu Thr Asp Pro Glu Ser Ala
217 1          5          10          15
218 Arg Gly Lys Leu Leu Gln Thr Ala Ala His Leu Phe Arg Asn Lys Gly
219          20          25          30
220 Phe Glu Arg Thr Thr Val Arg Asp Leu Ala Ser Ala Val Gly Ile Gln
221          35          40          45
222 Ser Gly Ser Ile Phe His His Phe Lys Ser Lys Asp Glu Ile Leu Arg
223          50          55          60
224 Ala Val Met Glu Glu Thr Thr His Tyr Asn Thr Ala Met Met Arg Ala
225 65          70          75          80
226 Ser Leu Glu Glu Ala Ser Thr Val Arg Glu Arg Val Leu Ala Leu Ile
227          85          90          95
228 Arg Cys Lys Leu Gln Ser Ile Met Gly Gly Ser Gly Glu Ala Met Ala
229          100          105          110
230 Val Leu Val Tyr Glu Trp Arg Ser Leu Ser Ala Glu Gly Gln Ala His
231          115          120          125
232 Val Leu Ala Leu Arg Asp Val Tyr Glu Gln Ile Trp Leu Gln Val Leu
233          130          135          140
234 Gly Glu Ala Lys Ala Ala Gly Tyr Ile Arg Gly Asp Val Phe Ile Thr
235 145          150          155          160
236 Arg Arg Phe Leu Thr Gly Ala Leu Ser Trp Thr Thr Thr Trp Phe Arg
237          165          170          175
238 Ala Gln Gly Ser Leu Thr Leu Glu Glu Leu Ala Glu Glu Ala Leu Leu
239          180          185          190

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241      195
244 <210> SEQ ID NO: 6
245 <211> LENGTH: 17
246 <212> TYPE: DNA
247 <213> ORGANISM: P. fluorescens
249 <400> SEQUENCE: 6
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252 <210> SEQ ID NO: 7
253 <211> LENGTH: 187
254 <212> TYPE: PRT
255 <213> ORGANISM: P. aeruginosa
257 <400> SEQUENCE: 7
258 Met Ser Glu Gln Leu Ser Thr Arg Arg Cys Asp Thr Pro Leu Leu Gln
259 1      5      10      15
260 Ala Phe Val Asp Asn Arg Thr Ile Leu Val Lys Ile Ala Ala Arg Ile
261      20      25      30
262 Thr Gly Cys Arg Ser Arg Ala Glu Asp Val Val Gln Asp Ala Phe Phe
263      35      40      45
264 Arg Leu Gln Ser Ala Pro Gln Ile Thr Ser Ser Glu Lys Ala Gln Leu
265      50      55      60
266 Ser Tyr Leu Phe Gln Ile Val Arg Asn Leu Ala Ile Asp His Tyr Arg
267 65      70      75      80
268 Lys Gln Ala Leu Glu Gln Lys Tyr Ser Gly Pro Glu Glu Glu Gly Leu
269      85      90      95
270 Asn Val Val Ile Gln Gly Ala Ser Pro Glu Thr Ser His Ile Asn Tyr
271      100     105     110
272 Ala Thr Leu Glu His Ile Ala Asp Ala Leu Thr Glu Leu Pro Lys Arg
273      115     120     125
274 Thr Arg Tyr Ala Phe Glu Met Tyr Arg Leu His Gly Val Pro Gln Lys
275      130     135     140
276 Asp Ile Ala Lys Glu Leu Gly Val Ser Pro Thr Leu Val Asn Phe Met
277 145     150     155     160
278 Ile Arg Asp Ala Leu Val His Cys Arg Lys Val Thr Ala Glu Arg Gln
279      165     170     175
280 Gly Asp Asn Val Thr His Leu Ser Ala Arg Arg
281      180     185
284 <210> SEQ ID NO: 8
285 <211> LENGTH: 176
286 <212> TYPE: PRT
287 <213> ORGANISM: P. putida
289 <400> SEQUENCE: 8
290 Met Ala Glu Gln Leu Ser Thr Ser Lys Cys Asp Ser Pro Leu Leu Gln
291 1      5      10      15
292 Ala Phe Val Asp Asn Arg Ser Ile Leu Val Lys Ile Ala Ala Arg Ile
293      20      25      30
294 Thr Gly Cys Arg Ser Arg Ala Glu Asp Val Val Gln Asp Ala Phe Phe
295      35      40      45
296 Arg Leu Ser Ala Ala Pro Gln Ile Thr Ser Ser Phe Lys Ala Gln Leu

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Pm4968.txt

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L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10